

SEQUENCE LISTING

<110> Degussa-Hüls AG, Forschungszentrum Jülich GmbH

<120> Novel nucleotide sequences coding for the cdsA gene

<130> 000009 BT

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<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (200)..(1090)

<223> cdsA gene

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<221> RBS

<222> (187)..(195)

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gcaagagtgt ttggaagaat tttttcgaaa atgctggcac catcaacagt gacattgtta 180
gaaacttcaa ggagaaccc atg aat gaa ccg gag caa cat cac cgg tcc atg 232
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agg atg ccc aaa ccc aaa aat aat gcg ggt cga gat ctc aaa gct gcc 280
Arg Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala
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att gct gtg ggg atc gga ctg ggg gtc ctg gtt ctt ttg ggg att gtc 328
Ile Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val
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cta agc cca tgg ggt tgg tac atc ctc gtt gca ggt ttt atg gct gca 376
Leu Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala
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gca aca tgg gaa gtt ggt agc aga ctt aaa gaa ggc ggc tat cat ttg 424
Ala Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu
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cca ctg ccg att atg atc atc ggc ggt cag gca atc atc tgg ctg tca 472
Pro Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser
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tgg cca ttt ggc acg atg ggc att ttg gcg tct ttt gtg gcc act gtg 520

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Ser	His	Pro	Met	Ala	Pro	Leu	Val	Ser	Pro	Lys	Lys	Ser	Trp	Glu	Gly		
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acg	tgg	ttg	atc	ctg	agt	gtg	atc	agc	agc	tcg	tat	ccg	tcg			1090	
Thr	Trp	Leu	Ile	Leu	Ser	Val	Ile	Ser	Ser	Ser	Tyr	Pro	Ser				
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<213> Corynebacterium glutamicum

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35 40 45
Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val
50 55 60
Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met
65 70 75 80
Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr
85 90 95
Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr
100 105 110
Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu
115 120 125
Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe
130 135 140
Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro
145 150 155 160
Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp
165 170 175
Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala
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Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile
195 200 205
Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp
210 215 220
His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys
225 230 235 240
Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly
245 250 255
Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp
260 265 270
Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu
275 280 285
Ser Val Ile Ser Ser Ser Tyr Pro Ser
290 295